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SEQUENCE LISTING

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<150> EP 02022869.8
<151> 2002-10-14

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<170> PatentIn version 3.3

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<212> PRT
<213> Homo sapien

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Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
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Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
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35 40 45

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
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Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
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Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
85 90 95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
100 105 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
115 120 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
130 135 140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145 150 155 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
165 170 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
180 185 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
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<213> Mus musculus

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35 40 45

Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val
50 55 60

Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp
65 70 75 80

Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln
85 90 95

Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp
100 105 110

Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val
115 120 125

Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Met Thr
130 135 140

Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu
145 150 155 160

Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr
165 170 175

Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr
180 185 190

Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr
195 200 205

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Ser Phe Ser Arg Thr Pro Gly Lys
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Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
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Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser Asp Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys
115 120 125

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
130 135 140

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
145 150 155 160

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
165 170 175

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
180 185 190

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
195 200 205

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
210 215 220

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
225 230 235 240

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
245 250 255

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
260 265 270

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
275 280 285

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
290 295 300

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
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Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
115 120 125

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
145 150 155 160

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
165 170 175

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
180 185 190

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
195 200 205

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
210 215 220

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
225 230 235 240

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
245 250 255

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
260 265 270

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
275 280 285

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
290 295 300

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
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Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
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Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
340 345

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<212> DNA
<213> Homo sapien

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aagtgc	tcttggagtt	acaagttatt	tcacttgagt	ccggagatgc	aagtattcat	180
gatacagtag	aaaatctgat	catccttagca	aacaacagtt	tgtcttctaa	tggaatgta	240
acagaatctg	gatgcaaaga	atgtgaggaa	ctggaggaaa	aaaatattaa	agaattttg	300
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aacagcacgt	accgtgttgt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	300
aaggagtaca	agtgcaggt	ctccaacaaa	gccctccag	cccccatcga	gaaaaccatc	360
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	atcccggtat	420
gagctgacca	agaaccaggt	cagcctgacc	tgcctggta	aaggcttcta	tcccagcgac	480
atcgccgtgg	agtggagag	caatggcag	ccggagaaca	actacaagac	cacgcctccc	540
gtgctggact	ccgacggctc	cttcttcctc	tacagcaagc	tcaccgtgga	caagagcagg	600
tggcagcagg	ggaacgttctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	660
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aactgggtgg aaagaaatag ctactcctgt tcagtggtcc acgagggtct gcacaatcac	660
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aagtgc当地tc tcttggagtt acaagttatt tcacttgagt ccggagatgc aagtattcat	180
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tggaatgta	240
acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg	300
cagagtttg tacatattgt ccaaatgttc atcaacactt cggatcccaa atctgctgac	360
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gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	660
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<212> DNA
<213> artificial sequence

<220>
<223> DNA coding for fusion protein

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aagtgtttc tcttggagtt acaagttatt tcacttgagt ccggagatgc aagtattcat 180
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tggaatgta 240
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gggtcagtaa gagctccaca ggtatatgtc ttgcctccac cagaagaaga gatgactaag 780
aaacaggtca ctctgacctg catggtcaca gacttcatgc ctgaagacat ttacgtggag 840
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gatggttctt acttcatgta cagcaagctg agagtggaaa agaagaactg ggtggaaaga 960
aatagctact cctgttcagt ggtccacgag ggtctgcaca atcaccacac gactaagagc 1020
ttctcccgga ctccggtaa atgag 1045

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<213> Homo sapien

<400> 11

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gac	63
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<211> 72	
<212> DNA	
<213> Homo sapien	
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tcctgcctcg ga	72
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<211> 75	
<212> DNA	
<213> Homo sapien	
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gcagccactc aggga	75
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<212> DNA	
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<211> 69	
<212> DNA	
<213> Homo sapien	
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gggctcgct	69
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<211> 40	
<212> DNA	
<213> Homo sapien	
<400> 16	
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<210> 17	

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<211> 144
<212> DNA
<213> Homo sapien

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gcagggcttc ctaaaacaga agcc                                         144

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<211> 74
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<220>
<223> oligonucleotide

<400> 18
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tccactggtg acaa                                         74

<210> 19
<211> 74
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

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<211> 37
<212> DNA
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<220>
<223> oligonucleotide

<400> 21
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<210> 22
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<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 22
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tccactggtg acaactgggt gaatgtaata agtgattga aaaaaattga a 111

<210> 23
<211> 111
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 23
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gaccactgaa gacccactta cattattcac taaactttt ttaacttcta g 111

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<213> Homo sapien

<400> 24

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20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

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Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Asp Ser Phe Val His Ile Val Asp Met Phe Ile Asn
100 105 110

Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
115 120 125

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
145 150 155 160

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
165 170 175

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
180 185 190

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
195 200 205

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
210 215 220

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
225 230 235 240

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
245 250 255

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
260 265 270

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
275 280 285

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
290 295 300

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
305 310 315 320

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
325 330 335

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
340 345

<210> 25
<211> 347
<212> PRT
<213> artificial sequence

<220>
<223> mutated Fc

<400> 25

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20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Asp Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
115 120 125

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
130 135 140

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
145 150 155 160

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
165 170 175

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
180 185 190

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
195 200 205

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
210 215 220

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
225 230 235 240

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
245 250 255

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
260 265 270

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
275 280 285

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
290 295 300

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
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Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
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<211> 1108
<212> DNA
<213> Homo sapien

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catattgatg ctactttata tacggaaagt gatgttcacc ccagttgcaa agtaacagca 180
atgaagtgc ttctcttggaa gttacaagtt atttcacttg agtccggaga tgcaagtatt 240
catgatacag tagaaaatct gatcatccta gcaaacaaca gtttgtcttc taatggaaat 300
gtaacagaat ctggatgcaa agaatgtgag gaactggagg aaaaaaattt taaagaattt 360
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gagtgacca acaacggaa aacagagcta aactacaaga acactgaacc agtcctggac 960
tctgtatggtt cttacttcat gtacagcaag ctgagagtgg aaaagaagaa ctgggtggaa 1020
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<210> 27
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<212> DNA
<213> artificial sequence

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<220>
<223> nucleic acid for mutated Fc

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<220>
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